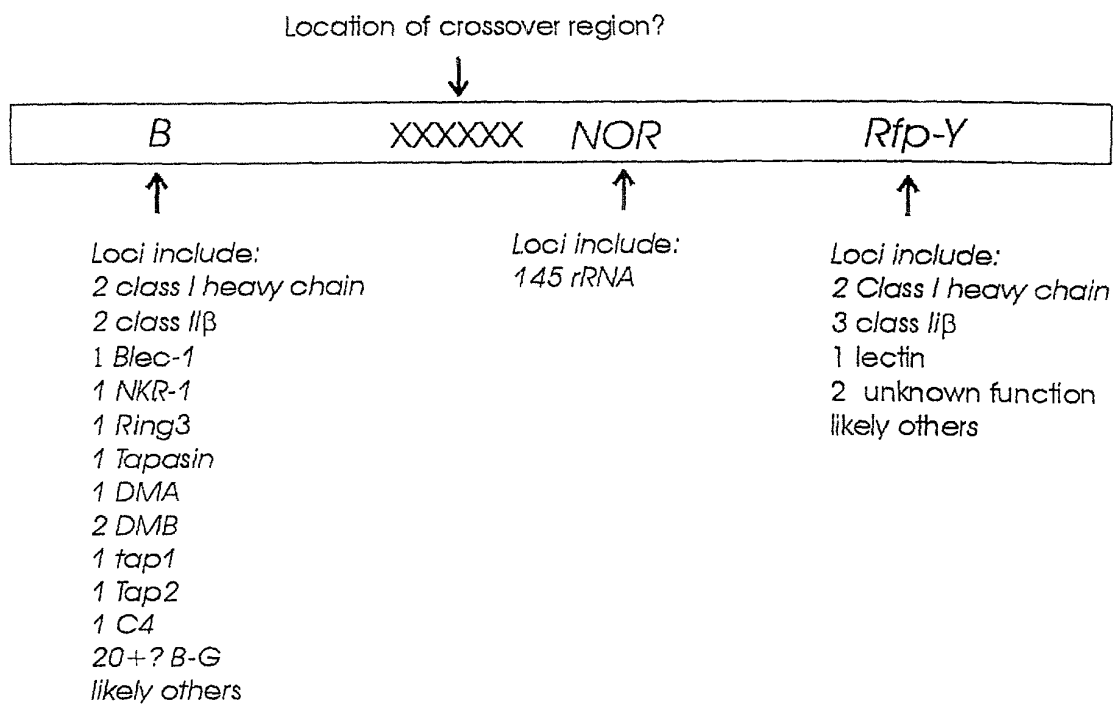


Figure 1



[illegible]

Figure 2B

[illegible]

Figure 3

α1 domain

YFV^w*7 10. 20. 30. 40. 50. 60. 70. 80.
GSHSLRYFLTCMTDPGPGMPRFVIVGVDDKIFGTYNKSRTAQPIVEMLPQEDQEHWDTQTQKAQGERDFDWNLRNRLPERYNKSK
BFIV*12 EL-T---IQ-A-----Q-W--T-----GEL-VH-N-TA-RYV-RT-WIAKA--QY--G---IG--N-QIDRE--GI-QR---QTG

α2 domain

YFV^w*7 90. 100. 110. 120. 130. 140. 150. 160. 170.
GSHTMQMMFGDILEDGSIRGYDQYAFDGRDFLAFDMDTMTFTAADPVAETKRRWETEGTYAERWKHELGTVCVQNLRRLRYLEHGKAALKRR
BFIV*12 ---V-W-Y-----G-P-----Y-M-Y-----T---KG-----V-E-VP---K--E-SE/P-----NY-EET---EW-----V-Y---E-G---

α3 domain

YFV^w*7 180. 190. 200. 210. 220. 230. 240. 250. 260. 270.
VQPEVRVWGKEADGILTLSCAHGFYRPRITISWMDGMVRDQETRWGGIVENS DGTYHASAAIDVLPEDGDKYWCRCVEHASLPQPGLFSW
BFIV*12 ER-----R-----V-V--L---A--G-DAHS-----G-----TWVT--AQ-G-----Q-----Y---

Transmembrane domain

YFV^w*7 280. 290. 300.
EP/QPNLIPIVAGAVVAIVAV/IAAVVGLVVWKS
BFIV*12 --P-----V-----VA-----IA-MVG--FIIYRRHA

Cytoplasmic domains

YFV^w*7 310. 320. 330.
GKEKKGYEAAAAGHDGESSGSATGSEPSI
BFIV*12 --KG---NI-PDRE-G--S-S---N-A-

Figure 4

GGTGTGGATTTCATCATCTACAGACGCCACGCAGGTAAAAGCAGAGGGGTGCAGGCGGGCAGTGGTGGCAGTGGGGGGATCTG
GGTCCCCCTTGGGAGCCCTCAGCCTGGCTGTGATGTGAACCTGTGTTGATTCATCTCTCTGTCTGCAGGGAAGAAGGGGAAGG
GCTACAACATCGCGCCCGGTGAGTGATGAGGGCAGCGCTGTCCCCACCTCTGCCCAGTGCCAGGGCGGTCTCTGGGTCTGCA
CTTCTCCCAGGGTACCCATTCTGGTGCTTGGGGCTGCTCCACGCCCCATAGGGAGCACAGGGCTGGGTCTCAGCTGTTC
CTCCCTTATAGACAGGGAAGGTGGATCCAGCAGCTCGAGCACAGGTGCGGTGTGGGGCTGTGGGTGGGAGGGGTCCGTGTGC
TCTCTGTGGTACTGCCAGGGCTGGGCTATGCTGGGGCTCTGCGGGGAGACCCCGGAGCAGAGGGTTGGGATGTGAACATGG
GCCCCGTGGGACACCATCTCTTCTCATCCCCACAGGGAGCAACCCCTCCATCTGAGTGCTGTGCTTCAGCATGCACGAAGCCA
ACAGTCCACACCAGCATTTGGGGTCAGTGATGGGCACAGCCCCATCCTCTTGACCTCTCACATCTCGTTCTGCTTCCTATGCT
GACTGTTATGC

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Figure 5

GGGGAGAAAGCGGGAGCTGCAGGTGGGGCCTGGACCCCTTGGGAATGCCCATGTTCTGACATGAGCTTAATGTTACACTTC
TTTCTATCTGTAGGGAAGGAGAAGAAGGGTTATGAAGCAGCGCCAGGTGAGTGCCAAGGGCAGCGCTTTACCCCTGCCAGTGCT
TGGGGTCAGGGCACTCTGGGGCCCCCTCGTTTGCTTTTGGGGTCACAGTGCAGGTGGTGGCATGATGCTCCATGCCCCACAGCGA
GCACAGAGCCAGGGCTCATGGCTCTCCCTCCCTTGCAGGCCAGGGCGGAGAATCCAGCATATCGGGCCACAGGTATAgTGTGGA
ATGGGGGTTTCAGGAGGGGTCCCTGTGGTTGGAGCATTCCAGtTCCTGCACTCCCCTGTTGGACCCACGGCCGGGGCAATAC
TGGGCCCcAaCCCTCCCTGGAGAAcCCCCAGGGTGGTGAGTCGGGACGGGGACGTGGTCCCATATGACACCACCTCTTCTCACC
CGCACAGGAAGTGAACCTCCCTTCTGAGTGCTGTGTTACTTCAGCCAGCCCTGCATGCATGTGTTTGGAGTGTGTGGGTGTGT
GTATCTCAGTGTGTGCTCAACTTCCTGCATCTCCTCGGGCTGACA

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Figure 6

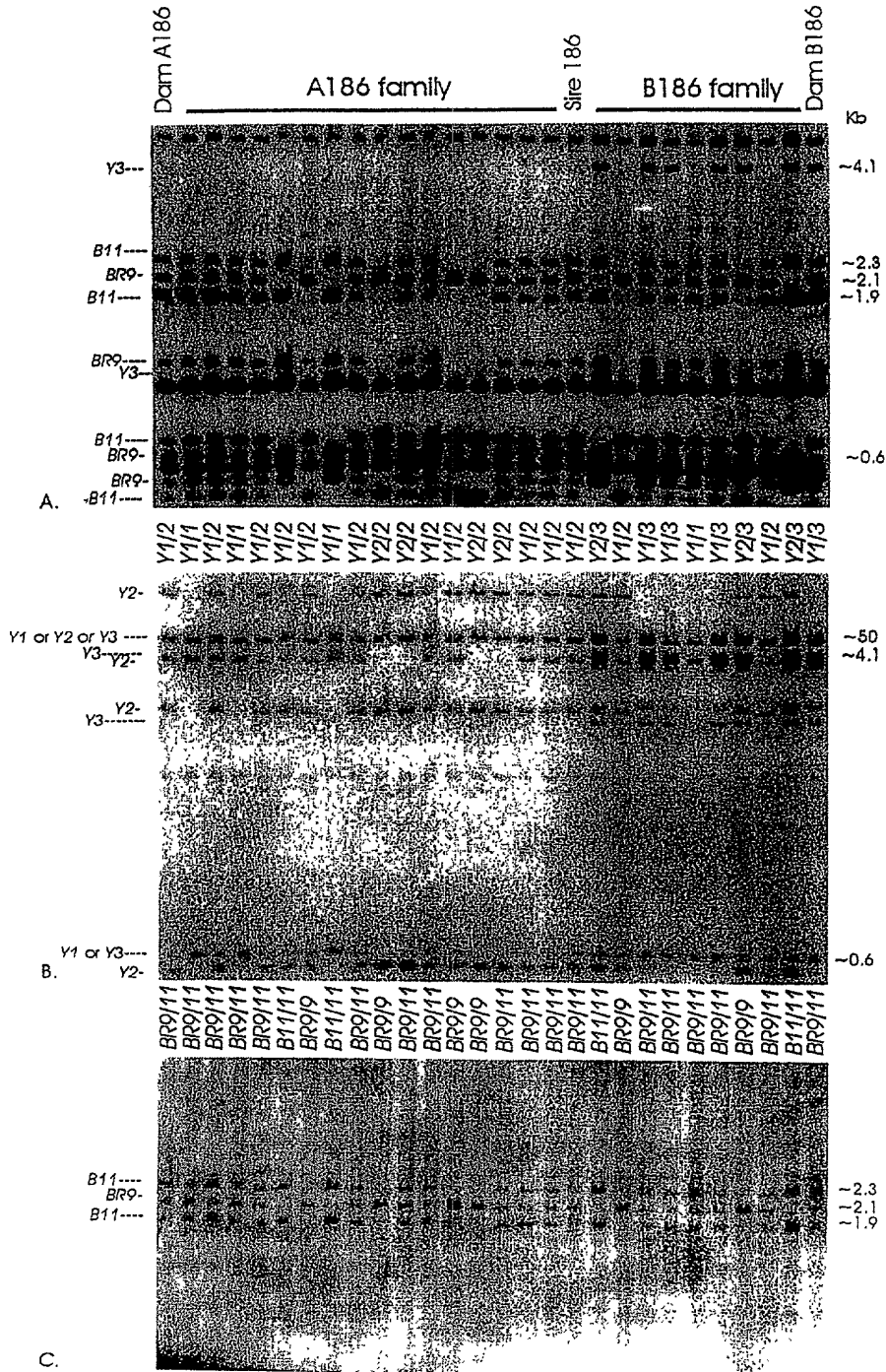


Figure 7

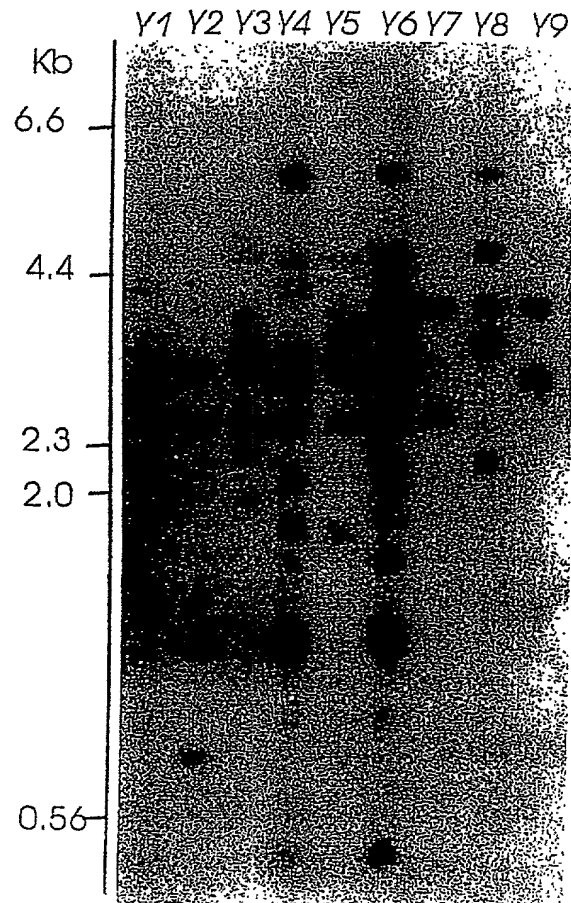


Figure 8

